<u>We claim:</u>

1. A method for identifying one or more genetic elements which selectively confer a target phenotype on a target cell, comprising:

    (i) generating a library of expression vectors comprising a variegated population of genetic elements from a population of genomic fragments;

    (ii) transfecting host cells with said library of expression vectors;

    (iii) subjecting the host cells to selective growth conditions under which genetic elements are expressed;

    (iv) isolating and/or amplifying a sub-population of host cells based on having the target phenotype during selective growth conditions;

    (v) differentially labeling and admixing genetic elements from said sub-population of host cells with genomic fragments and contacting the admixture with one or more oligonucleotide arrays; and

    (vi) identifying coding sequences which confer said phenotype by hybridization of said genomic sequences to said one or more oligonucleotide arrays.

2. A method for identifying one or more genetic elements which selectively confer a target phenotype on a target cell, comprising:

    (i) transfecting host cells with a library of expression vectors comprising a variegated population of coding sequences for genetic elements;

    (ii) subjecting the host cells to selective growth conditions under which said genetic elements are expressed;

    (iii) isolating and/or amplifying a sub-population of host cells based on having the target phenotype during selective growth conditions;

    (iv) contacting coding sequences for said genetic elements from said sub-population of host cells with one or more oligonucleotide arrays; and

    (v) identifying individual coding sequences which confer said phenotype by hybridization to said one or more oligonucleotide arrays.

3. The method of claim 2, wherein the variegated population of coding sequences for genetic elements includes a genomic fragment library.

4. The method of claim 2, wherein the variegated population of coding sequences for genetic elements includes a cDNA library.

5. The method of claim 2, wherein the host cell is a prokaryotic cell.

6. The method of claim 2, wherein the host cell is a eukaryotic cell.

7. The method of claim 6, wherein the host cell is a mammalian cell.

8. The method of claim 2, wherein the expression vector is an episomal vector.

9. The method of claim 2, wherein the expression vector is an intregrative vector.

10. The method of claim 2, wherein said target phenotype is a change in expression of a reporter gene.

11. The method of claim 2, wherein said target phenotype is a change in expression of a marker protein.

12. The method of claim 2, wherein said target phenotype is ability to growth under the selective conditions.

13. The method of claim 2, wherein said target phenotype is change in cell morphology.

14. The method of claim 2, wherein said sub-population of host cells is isolated by flow cytometry based on expression of a reporter gene or marker protein.

15. The method of claim 2, wherein said genetic elements encode polypeptides.

16. The method of claim 2, wherein said genetic elements encode antisense RNA.

17. A method of conducting a drug discovery business comprising:

(i) identifying, by the assay of claim 2, a target gene which confers said target phenotype;

(ii) identifying agents by their ability to inhibit expression of the target gene or the activity of an expression product of the target gene in order to inhibit said target phenotype in a target cell or tissue;

(iii) conducting therapeutic profiling of agents identified in step (b), or further analogs thereof, for efficacy and toxicity in animals; and

(iv) formulating a pharmaceutical preparation including one or more agents identified in step (iii) as having an acceptable therapeutic profile.

18. The method of claim 17, including an additional step of establishing a distribution system for distributing the pharmaceutical preparation for sale, and may optionally include establishing a sales group for marketing the pharmaceutical preparation.

19. A method of conducting a target discovery business comprising:

(i) identifying, by the assay of claim 2, one or more target genes which confer said target phenotype;

(ii) (optionally) conducting therapeutic profiling of the loss-of-function phenotypes of said target gene for potential efficacy and toxicity in animals; and

(iii). licensing, to a third party, the rights for further drug development of inhibitors of said target gene(s).